NUCLEIC ACID ENZYME FOR RNA CLEAVAGE

This application is a continuation of
PCT/CA99/00391, filed April 29, 1999, which claims priority to
Canadian patent application 2,230,203, filed April 29, 1998,
5 both of which are incorporated herein in their entirety.

TECHNICAL FIELD

The invention relates to a novel ribozyme
construction for the specific recognition and cleavage of RNA,
and biotechnological as well as therapeutic uses thereof.

10 ### BACKGROUND ART

Though enzymatic activity has long been considered
the exclusive domain of proteins, discoveries in molecular
biology over the past couple of decades have led to the
realization that ribonucleic acid (RNA) can also function as
15 an enzyme. RNA enzymes are often referred to as ribozymes.

Ribozyme substrates are generally confined to RNA
molecules, and enzymatic activities of ribozymes include the
cleavage and/or ligation of RNA molecules. The cleavage
activity may be intramolecular, known as *cis*-acting or
20 intermolecular, known as *trans*-acting. There are at least
five classes of ribozymes known, including Group I introns,
Group II introns, hammerhead, hairpin, and delta ribozymes.
The last three are derived from plant satellites and viroids.

Since 1982, several unexpected diseases caused by
25 RNA-based pathogenic agents have emerged. These include the
lethal Acquired Immune Deficiency Syndrome (AIDS) and delta
hepatitis, a particularly virulent form of fulminant hepatitis
caused by a viroid-like RNA agent. These blood-borne diseases
are spread at the RNA level, manifest themselves in cells of
30 patients, and are by now present within the bloodstream of
millions of individuals. Conventional biotechnology, with its
reliance on recombinant DNA methods and DNA-level intervention
schemes, has been slow to provide valid approaches to combat
these diseases.

Two forms of *delta* ribozymes, namely genomic and antigenomic, are derived, and referred to by, the polarity of the hepatitis delta virus (HDV) genome from which the ribozyme is generated. Like hammerhead and hairpin ribozymes, the

5   *delta* ribozymes cleave a phosphodiester bond of their RNA substrates and give rise to reaction products containing a 5'-hydroxyl and a 2',3'-cyclic phosphate termini. They are metalloenzymes and a low concentration (<1 mM) of magnesium (Mg^{2+}) or calcium (Ca^{2+}) is required for *delta* ribozyme

10 cleavage. Both genomic strand and antigenomic strand forms exhibit self-cleavage activity, and it has been suggested that they are involved in the process of viral replication (Lazinski, D. W., and Taylor, J. M. (1995) *RNA* **1**, 225-233).

Delta ribozymes derived from the genome of HDV are

15 of interest in the development of a gene regulation system in which the designed ribozymes would down-regulate the expression of a target gene. The facts that *delta* ribozymes are derived from HDV and that this pathogen naturally replicates in animal systems, suggest that this catalytic RNA

20 could be used to control gene expression in human cells. Like other ribozymes, the designed ribozyme should specifically cleave its target substrates while leaving other cellular RNA molecules intact.

Trans-acting ribozymes carry out intermolecular

25 cleavage activity. Some trans-acting *delta* ribozymes have been developed by removing a single-stranded junction which connects the catalytic portion to the substrate portion in *cis*-acting *delta* ribozymes. This results in two separate molecules, one possessing the substrate sequence and the other

30 the catalytic property (Been, M.D. and Wichhan, G.S. (1997) *Eur. J. Biochem.*, **247**, 741-753). Interactions between such *delta* ribozymes and the substrate occur through the formation of a helix, referred as the P1 stem. However, the example of the trans-acting ribozyme disclosed by Been et al. (supra) was

35 not useful for cleaving long substrate molecules, such as those having therapeutic applications.

In United States Patent No. 5,225,337, issued on

July 6, 1993 in the names of Hugh D. Robertson et al., there
are disclosed ribozymes derived from a specific domain present
in the HDV RNA for specifically cleaving targeted RNA
sequences and uses thereof for the treatment of disease

5   conditions which involve RNA expression, such as AIDS. These
ribozymes consist of at least 18 consecutive nucleotides from
the conserved region of HDV isolates between residues 611 and
771 on the genomic strand and between residues 845 and 980 on
the complementary antigenomic strand. These ribozymes are

10   proposed to fold into an axe-head model secondary structure
(Branch, A. D., and Robertson, H. D. (1991) *Proc. Natl .Acad.
Sci. USA* **88**, 10163-10167). The ribozymes developed according
to this model structure require the substrate to be bound to
the ribozyme through the formation of two helices, one located

15   on either side of the cleavage site. Further, such ribozymes
apparently require a 12-15 nucleotide recognition sequence in
the substrate in order to exhibit the desired activity. Such
a long recognition sequence is not practical in the
development of therapeutic or diagnostic applications.

20   In United States Patent No. 5,625,047, issued on
April 29, 1997 in the names of Michael D. Been et al., there
are disclosed enzymatic RNA molecules proposed to fold into a
pseudoknot model secondary structure (discussed below). The
method disclosed for the development of efficient ribozymes

25   requires a short recognition sequence of only 7 to 8
nucleotides in the substrate, a preference for a guanosine
base immediately 3' to the cleavage site, a preference for U,
C or A immediately 5' to the cleavage site, and the
availability of a 2'-hydroxyl group for cleavage to occur.

30   Thus, the specificity of recognition of these ribozymes is
limited to 6 or 7 base pairing nucleotides with the substrate
and a preference of the first nucleotide located 5' to the
cleavage site. Neither tertiary interaction(s) between the
base paired nucleotides and another region of the ribozyme,

35   nor single-stranded nucleotides are involved to define the
specificity of recognition of these ribozymes. Because the
recognition features are limited, these ribozymes have a

limited specificity, and thus, are not practical for further clinical or biotechnical applications.

A pseudoknot-like structure for *delta* ribozymes has been proposed by Perrotta and Been (Perrotta, A. T., and Been, M. D. (1991) *Nature* **350**, 434-436). This model structure consists of two stems (P1 and P2), two stem-loops (P3 and P4) and three single-stranded regions (J1/2, J1/4 and J4/2). An additional stem, named P1.1, has been formed by two GC base pairs between nucleotides from the J1/4 junction and the P3 loop (Ferré-D'Amaré, A.R., Zhou, K. and Doudna, J.A. (1998) *Nature*, **350**, 434-436).

It would be highly desirable to be provided with a novel *delta* ribozyme for the cleavage of both small and large RNA substrates for which the specificity of recognition is well defined. Such specificity would yield optimal conditions for further therapeutical and biotechnological developments of *delta* ribozymes.

SUMMARY OF THE INVENTION

One aim of the present invention is to provide a novel delta ribozyme for the cleavage of RNA substrates for which the specificity is defined by a domain composed of at least 7 nucleotides. It is also an aim to provide a method for the development of such ribozymes.

In one aspect, the invention provides a method for cleaving a nucleic acid substrate with a nucleic acid enzyme at a cleavage site comprising mixing the substrate with the enzyme, wherein the substrate includes a 7 nucleotide sequence with at least 6 nucleotides 3' to the cleavage site and at least 1 nucleotide 5' to the cleavage site of formula:

$$5'-H' \ GNNHNN-3'$$

wherein each

N is a nucleotide which may be the same or different,

H is a nucleotide selected from the group consisting of A, U, C, and T, and

is the site of cleavage, and

H' is a ribonucleotide selected from the group consisting of A, U, and C,

wherein

(i) the first nucleotide 3' to the cleavage site is capable of forming a wobble pair with the enzyme,

(ii) the second, third, fifth, and sixth nucleotides 3' to the cleavage site are capable of forming conventional Watson-Crick base pairs with the enzyme,

(iii) the fourth nucleotide 3' to the cleavage site is capable of forming a triplet with the enzyme comprising a non-conventional Watson-Crick base pair and a conventional Watson-Crick base pair, and

(iv) the ribonucleotide directly 5' to the cleavage site does not form a base pair with the enzyme; and

the enzyme comprises a substrate binding portion which is capable of base pairing to the 6 nucleotides 3' to the cleavage site of the substrate and which binding portion comprises the sequence:

$$3'-UNNXNN-5'$$

wherein each

N is a nucleotide which may be the same or different, and

X is a nucleotide selected from the group consisting of T, U, A, and G,

whereby binding of the substrate to the enzyme effects cleavage of the substrate at the cleavage site.

In another aspect, the invention provides a nucleic acid enzyme capable of recognizing and cleaving a nucleic acid substrate at a cleavage site comprising a substrate binding portion which is capable of base pairing to the 6 nucleotides 3' to the cleavage site of the substrate and which binding portion comprises the sequence:
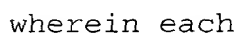
$$3'-UNNXNN-5'$$

wherein each

  N is a nucleotide which may be the same or different, and

  X is a nucleotide selected from the group consisting of

  T, U, A, G, and

5 the substrate includes a 7 nucleotide sequence with at least 6
nucleotides 3' to the cleavage site and at least 1 nucleotide
5' to the cleavage site of formula:

       5'- H' GNNHNN-3'

10

wherein each

  N is a nucleotide which may be the same or different,

  H is a nucleotide selected from the group consisting of

  A, U, C, and T,

15   is the site of cleavage, and

  H' is a ribonucleotide selected from the group consisting

  of A, U, and C,

wherein

  (i) the first nucleotide 3' to the cleavage site is

20 capable of forming a wobble pair with the enzyme,

  (ii) the second, third, fifth, and sixth nucleotides 3'
to the cleavage site are capable of forming conventional
Watson-Crick base pairs with the enzyme,

  (iii) the fourth nucleotide 3' to the cleavage site is

25 capable of forming a triplet with the enzyme comprising a non-
conventional Watson-Crick base pair and a conventional Watson-
Crick base pair, and

  (iv) the first ribonucleotide directly 5' to the cleavage
site does not form a base pair with the enzyme.

30 **BRIEF DESCRIPTION OF THE DRAWINGS**

   Figure 1 illustrates the secondary structure and
nucleotide sequences of two trans-acting antigenomic *delta*
ribozymes of the invention and complementary substrates; panel
A is the secondary structure of the complex formed between

35 δRzP1.1 and a substrate Sp1.1; panel B is the P1 region of the

complex formed between δRzP1.2 and a substrate Sp1.2; the rest
of the structure is identical to δRzP1.1 as in panel A;

Figure 2 illustrates the secondary structure of a
ribozyme in accordance with the invention, with an ultrastable
5   L4 loop; in the inset is the sequence of a 14-nucleotide long
substrate;

Figure 3 illustrates the secondary structure of a
ribozyme in accordance with the invention; the inset shows the
ultrastable L4 loop;

10   Figure 4 shows a two-dimensional representation of a
catalytic trimolecular complex (RzA: RzB:S) of the invention;

Figure 5 shows results from Example 3, namely
comparative analyses of the cleavage reactions catalyzed by
delta ribozymes;

15   Figure 6 shows a two-dimensional representation of a
catalytic trimolecular complex (RzA: RzB:S); the influence of
2'-OH groups individually at positions 9 to 15 on RzB by
replacing the ribonucleotide at these positions with the
corresponding deoxy-ribonucleotide is shown; the symbol –
20   represents a two-fold diminution of activity compared to an
unmodified RzB while the symbol = represents an unchanged
catalytic activity; symbols + and ++ respectively represent an
increased activity of 1.5- and 2- fold; horizontal bars
represent base pairs; wobble and homopurine base pairs are
25   respectively represented by one and two ovals; the arrow
indicates the site of catalytic cleavage;

Figure 7 shows in Panel A the structural and
functional features of virion DNA, including the viral direct
repeat (DR) sequences (boxed), and the protein ($\bullet$) and RNA
30   ($\wedge\wedge\wedge$) species found at the 5' ends of the minus and plus DNA
strands, respectively; the dashed line indicates the presence
of the single stranded gap; the RNA products are depicted by
wavy lines; the target area is located in pre-S2 and S
regions, and is indicated by the scissors symbol; panel B
35   illustrates the secondary struction of an engineered ribozyme
of the the invention, such that the substrate binding region

is 5'GGGAUAU-3', complementary to HBV mRNA substrates; the recognition site on the mRNA is located on the pres-S2 and S mRNA (2.1 kb, as shown in Panel A); the arrow indicates the cleavage site.

5   **DESCRIPTION OF THE PREFERRED EMBODIMENTS OF THE INVENTION**

The subject invention provides for a method of designing selective nucleic acid enzymes, such that a nucleic acid substrate is cleaved at a specified cleavage site by the nucleic acid enzyme. This method includes the selection of

10   certain substrate sequences and, within the enzymes, certain substrate binding sequences, such that efficient cleavage at a specified site in the nucleic acid substrate can take place. The subject invention also provides for nucleic acid enzymes designed using such method.

15   For the purpose of the present invention the following abbreviations are defined: "A" is a nucleotide comprising adenine including both the ribo- and deoxyribo-forms; "G" is a nucleotide comprising guanine including both the ribo- and deoxyribo-forms; "C" is a nucleotide comprising

20   cytidine including both the ribo- and deoxyribo-forms; "U" is a nucleotide comprising uracil; "T" is a nucleotide comprising thymine; "R" is a nucleotide comprising purine, which purine is selected from the group consisting of A and G; and "Y" is a nucleotide comprising pyrimidine, which pyrimidine is

25   selected from the group consisting of U, C, and T.

Selection of Substrate Sequence

Substrate nucleic acid includes any nucleic acid sequence which can act as a substrate for a nucleic acid enzyme of the invention. As such it includes ribonucleotides,

30   deoxyribonucleotides, or mixtures of both. Nucleotides may also include synthetic or modified nucleotides.

The nucleic acid enzymes of the invention can be used to target a large number of nucleic acid substrates so long as certain conditions of the recognition mechanism are

35   met. The nucleic acid substrate must include a 7 nucleotide

sequence with at least 6 nucleotides 3' to the cleavage site and at least 1 nucleotide 5' to the cleavage site of formula:

$$5'-H' \ GNNHNN-3'$$

5

wherein each

    N is a nucleotide which may be the same or different,

    H is a nucleotide selected from the group consisting of A, U, C, and T, and

10   is the site of cleavage, and

    H' is a ribonucleotide selected from the group consisting of A, U, and C.

     The first nucleotide 3' to the cleavage site is capable of forming a wobble pair with the enzyme. The wobble
15 base pair (G-U) at the cleavage site is required to maintain a high level of cleavage. Conventional Watson-Crick base pairs such as A-U and G-C, as well as mismatches at this position decrease the cleavage activity.

     The second, third, fifth, and sixth nucleotides 3'
20 to the cleavage site are capable of forming conventional Watson-Crick base pairs with the enzyme.

     The fourth nucleotide 3' to the cleavage site is capable of forming a conventional Watson-Crick base pair with the substrate binding region of the enzyme. Additionally,
25 such base pair interacts with a nucleotide elsewhere in the ribozyme (i.e. the nucleic acid enzyme) to form a triplet by means of a non-conventional Watson-Crick base pair. Non-conventional Watson-Crick base pairs include Hoogsteen pairs and reversed-Hoogsteen pairs. The position requires an A, U,
30 or C.

     The ribonucleotide directly 5' to the cleavage site does not form a base pair with the ribozyme.

     Preferably, the substrate molecule does not contain two consecutive pyrimidine nucleotides directly 5' to the
35 cleavage site.

In another preferred aspect, the substrate comprises the sequence 5'-H' GNNHNNN-3', more preferably the sequence 5'-NNRH' GNNHNNN-3', wherein R is G or A.

In one embodiment, the substrate preferably comprises the sequence 5'-RRRH' GNNHNNN-3'. More preferably, such sequence is selected from the group consisting of 5'-GGGC GNNUNNN-3', 5'-GGGC GNNCNNN-3', 5'-GGGU GNNUNNN-3', 5'-GGGU GNNCNNNN-3', and 5'-AAAC GNNUNNN-3'.

In another embodiment, the substrate preferably comprises the sequence 5'-YHRH' GNNHNNN-3', wherein Y is C, U, or T. It is preferred that the four nucleotides directly 5' to the cleavage site are chosen such that Y is C or U, preferably C; H is one of U, C, or A, preferably U or C, more preferably U; R is preferably A; and H is A, C, or U, preferably A or C, more preferably A.

It is preferable that the four nucleotides directly 5' to the cleavage site do not form a hairpin structure.

Selection of Ribozyme Sequence

By ribozymes, it is meant a nucleic acid enzyme, in other words any nucleic acid sequence having enzymatic activity, i.e. the ability to catalyze a reaction. As such it includes nucleic acid sequences made up of ribonucleotides, deoxyribonucleotides, or mixtures of both. Nucleotides may also include synthetic or modified nucleotides.

The selection of the sequence of the substrate binding region of the ribozyme, should be done such that the binding region comprises the sequence 3'-UNNXNN-5', wherein each N is a nucleotide which may be the same or different, and X is a nucleotide selected from the group consisting of T, U, A, and G.

The invention preferably provides for a nucleic acid enzyme with a secondary structure which comprises three or more distinct double-stranded regions, or stem-regions. This includes regions of base-pairing which may or may not be capped by a single-stranded loop, to form a stem-loop region. Preferably, the nucleic acid ribozyme includes two or more distinct single-stranded regions, one of which includes a

substrate binding region which will base pair to the
substrate.   More preferably there are two single stranded
regions.

          The invention preferably contemplates the use of
5   nucleic acid enzymes derived from hepatitis delta virus, known
as *delta* ribozymes.

Generation of Ribozyme and Substrate

          Trans-acting *delta* ribozymes of the invention were
generated based on the pseudoknot-like structure proposed by
10   Perrotta and Been, by removing the single-stranded region
(region J1/2) located at the junction between the P1 and P2
stems.   In addition, the P2 stem was elongated, by
introducing, for instance, three G-C base pairs, and by
shortening the P4 stem.

15   Figure 1 illustrates an example of two ribozymes,
δRzP1.1 and δRzP1.2, in accordance with one aspect of the
invention.   The base paired regions of the pseudoknot-like
structure are numbered according to Perrotta and Been
(Perrotta, A. T., and Been, M. D. (1991) *Nature* **350**, 434-436).
20   The dashed line represents the J1/2 single-stranded region
joining the substrate and ribozyme molecules present in the
cis-form.   This single-stranded area was eliminated to produce
a trans-acting ribozyme of the invention.   The arrow indicates
the cleavage site.   The homopurine basepair at the top of the
25   P4 stem is represented by two dots (**G• •G**), while the wobble

base pair is represented by a single dot (**G•U**).   The two small
dotted lines illustrate the P1.1 stem formed by two GC base
pairs.

          In another aspect, the invention provides for a
30   ribozyme with an elongated P2 stem and shortened P4 stem,
which further comprises a modification of the L4 loop.
Figures 2 and 3 show ribozymes in accordance with this
embodiment.   S and Rz represent substrate and ribozyme
respectively.

35   In one aspect, the invention provides for a
bimolecular ribozyme.   This may be achieved by removal of the

L4 loop. Figure 4 shows a ribozyme in accordance with this embodiment.

Applications

Ribozyme activity can be optimized by chemically
5   synthesizing ribozymes with modifications that prevent their
degradation by serum ribonucleases (see e.g., Eckstein et al.,
International Publication No. WO 92/07065; Perreault et al.,
Nature 1990, 344:565; Pieken et al., Science 1991, 253:314;
and Chowrira et al., 1993 J. Biol. Chem. 268, 19458, which
10   describe various chemical modifications that can be made to
the sugar moieties of enzymatic RNA molecules, all of which
publications are incorporated by reference herein),
modifications which enhance their efficacy in cells, and
removal of helix-containing bases to shorten RNA synthesis
15   times and reduce chemical requirements.

In one aspect, the invention provides a substrate
molecule which is a target RNA, such as a viral RNA, or an RNA
crucial to the life cycle of a pathogen, or an RNA manifested
as a result of an inherited disease, based on the substrate
20   specificity described herein.

Ribozymes are added directly, or can be complexed
with cationic lipids, packaged within liposomes, or otherwise
delivered to target cells. The RNA or RNA complexes can be
locally administered to relevant tissues *ex vivo*, or *in vivo*
25   through injection, aerosol inhalation, infusion pump or stent,
with or without their incorporation in biopolymers.

Sullivan, et al., (WO 94/02595, incorporated by
reference herein), describes general methods for delivery of
enzymatic RNA molecules. Ribozymes may be administered to
30   cells by a variety of methods known to those familiar to the
art, including, but not restricted to, encapsulation in
liposomes, by iontophoresis, or by incorporation into other
vehicles, such as hydrogels, cyclodextrins, biodegradable
nanocapsules, and bioadhesive microspheres. For some
35   indications, ribozymes may be directly delivered *ex vivo* to
cells or tissues with or without the aforementioned vehicles.
Alternatively, the RNA/vehicle combination is locally

delivered by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill

5   form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of ribozyme delivery and administration are provided in Sullivan, et al., ("Method and Reagent for Treatment of Arthritic Conditions" U.S.S.N. 08/152,487, filed November 12, 1993, and incorporated

10   by reference herein).

         Another means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for

15   eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory

20   sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein, O. and Moss, B., 1990, Proc. Natl. Acad. Sci. U S A, 87, 6743-7; Gao, X. and Huang;, L.,

25   1993, Nucleic Acids Res., 21, 2867-72; hereby incorporated by reference). Several investigators have demonstrated that ribozymes expressed from such promoters can function in mammalian cells (e.g. Kashani-Sabet, M., et al., 1992, Antisense Res. Dev., 2, 3-15; Ojwang, J. O., et al., 1992,

30   Proc. Natl. Acad. Sci. U S A, 89, 10802-6; hereby incorporated by reference). The above ribozyme transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or

35   adeno-associated vectors), or viral RNA vectors (such as retroviral, Semliki forest virus, hepatitis *delta* virus, and sindbis virus vectors).

Thus, ribozymes of the present invention that cleave target mRNA and thereby inhibit and/or reduce target activity have many potential therapeutic uses, and there are reasonable modes of delivering the ribozymes in a number of the possible

5   indications.

By "inhibit" is meant that the activity or level of target RNA is reduced below that observed in the absence of the ribozyme, and preferably is below that level observed in the presence of an inactive RNA molecule able to bind to the

10   same site on the RNA, but unable to cleave that RNA.

By "vectors" is meant any nucleic acid and/or viral-based construct used to deliver a desired nucleic acid.

Examples

15   **Example 1:   Preparation of Ribozymes, Substrates, and Plasmids.**

Construction of plasmids carrying ribozymes of the invention. The antigenomic ribozyme sequence of the hepatitis *delta* virus described by Makino *et al* (Makino, S. et al.

20   (1987) *Nature* **329**, 343-346, hereby incorporated by reference) was used as the basis for generating trans-acting *delta* ribozymes of the invention. Briefly, the construction was performed as follows. Two pairs of complementary and overlapping oligonucleotides, representing the entire length

25   of the ribozyme (57 nt), were synthesized and subjected to an annealing process prior to cloning into pUC19. The annealed oligonucleotides were ligated to *Hind*III and *Sma*I co-digested pUC19 to give rise to a plasmid harboring the delta ribozyme (referred to as pδRzP1.1). The minigene was designed so as to

30   have unique SphI and SmaI restriction sites. The sequence of the T7 RNA promoter was included at the 5′ end of the ribozyme so as to permit *in vitro* transcription. Variations based on this "wild type" ribozyme are constructed by replacing the *Sph*I-*Sma*I fragment of pδRzP1.1 by an oligonucleotide duplex

35   containing the desired sequence. The sequences of engineered ribozymes were confirmed by DNA sequencing. Plasmids contain-

ing wild type and mutant ribozymes were then prepared using
Qiagen tip-100 (Qiagen Inc.), digested with *SmaI*, purified by
phenol and chloroform extraction and precipitated for further
use as templates for in vitro transcription reactions.

5   *Synthesis of Ribozymes and Substrates. Ribozyme:*
In vitro transcription reactions contained 5 μg linearized
recombinant plasmid DNA as template, 27 units RNAGuard (RNase
inhibitor (Pharmacia), 4 mM of each rNTP (Pharmacia), 80 mM
HEPES-KOH pH 7.5, 24 mM $MgCl_2$, 2 mM spermidine, 40 mM DTT, 0.01

10   unit Pyrophosphatase (Boehringer Mannheim) and 25 μg purified
T7 RNA polymerase in a final volume of 50 μL, and were
incubated at 37°C for 4 hr. *Substrates*: Deoxyoligonucleotides
(500 pmoles) containing the substrate and the T7 promoter
sequence were denatured by heating at 95°C for 5 min in a 20

15   μL mixture containing 10 mM Tris-HCl pH 7.5, 10 mM $MgCl_2$, 50 mM
KCl_2, and allowed to cool slowly to 37°C. The *in vitro*
transcription reactions were carried out using the resulting
partial duplex formed as template under the same conditions as
described for the production of the ribozyme.

20   After incubation, the reaction mixtures were
fractionated by denaturing 20% polyacrylamide gel electro-
phoresis (PAGE, 19:1 ratio of acrylamide to bisacrylamide)
containing 45 mM Tris-borate pH 7.5, 7 M urea and 1 mM EDTA.
The reaction products were visualized by UV shadowing. The

25   bands corresponding to the correct sizes of either ribozymes
or substrates were cut out, and the transcripts eluted
overnight at 4°C in a solution containing 0.1% SDS and 0.5 M
ammonium acetate. The transcripts were then precipitated by
the addition of 0.1 vol 3 M sodium acetate pH 5.2 and 2.2 vol

30   ethanol. Transcript yield was determined by
spectrophotometry.

     Synthesis and Purification of RNA and RNA/DNA Mixed
Polymer: RNA and RNA-DNA mixed polymers were sythesized on an
automated oligonucleotide synthesizer, and deprotected accord-

35   ing to previously described procedures (Perreault, J.P., and
Altman, S. (1992) J. Mol. Biol. 226, 339-409 hereby incorpor-

ated by reference). These polymers were purified by 20% PAGE.
Major bands were excised and eluted as described above.

End-labelling of RNA with [Y-32P]ATP. Purified
transcripts (10 pmoles) were dephosphorylated in a 20 μL

5   reaction mixture containing 200 mM Tris-HCl pH 8.0, 10 units
RNA guard, and 0.2 unit calf intestine alkaline phosphatase
(Pharmacia). The mixture was incubated at 37°C for 30 min,
and then extracted twice with a same volume of
phenol:chloroform (1:1). Dephosphorylated transcripts (1

10   pmole) were end-labelled in a mixture containing 1.6 pmole [Y-
32P]ATP, 10 mM Tris-HCl pH 7.5, 10 mM $MgCl_2$, 50 mM KCl and 3
units T4 polynucleotide kinase (Pharmacia) at 37°C for 30 min.
Excess [Y-32P]ATP was removed by applying the reaction mixture
onto a spin column packed with a G-50 Sephadex gel matrix

15   (Pharmacia). The concentration of labelled transcripts was
adjusted to 0.01 pmol per mL by the addition of water.

Example 2: Kinetics

Cleavage reactions. To initiate a cleavage

20   reaction, various concentrations of ribozymes were mixed with
trace amounts of substrate (final concentration <1 nM) in a 18
μL reaction mixture containing 50 mM Tris-HCl pH 7.5, and
subjected to denaturation by heating at 95°C for 2 min. The
mixtures were quickly placed on ice for 2 min and equilibrated

25   to 37°C for 5 min prior to the initiation of the reaction.
Unless stated otherwise, cleavage was initiated by the
addition of $MgCl_2$ to 10 mM final concentration. The cleavage
reactions were incubated at 37°C, and followed for 3.5 hours
or until the endpoint of cleavage was reached. The reaction

30   mixtures were periodically sampled (2-3 μL), and these samples
were quenched by the addition of 5 μL stop solution containing
95% formamide, 10 mM EDTA, 0.05% bromophenol blue and 0.05%
xylene cyanol. The resulting samples were analyzed by a 20%
PAGE as described above. Both the substrate and the reaction

35   product bands were detected using a Molecular Dynamic

radioanalytic scanner after exposition of the gels to a
phosphoimaging screen.

Kinetic analysis. Measurement of pseudo-first-order
rate constant (k_{cat}, K_M and k_{cat}/K_M) were performed under single

5   turnover conditions. Briefly, trace amounts of end-labelled
substrate (<1 nM) were cleaved by various ribozyme
concentrations (5 to 500 nM). The fraction cleaved was
determined, and the rate of cleavage (k_{obs}) obtained from
fitting the data to the equation $At = A\infty(1-e^{-kt})$ where At is

10   the percentage of cleavage at time t, $A\infty$ is the maximum
percent cleavage (or the end point of cleavage), and k is the
rate constant (k_{obs}). Each rate constant was calculated from
at least two measurements. The values of k_{obs} obtained were
then plotted as a function of ribozyme concentrations for

15   determination of the other kinetic parameters: k_{cat}, K_M and
k_{cat}/K_M. Values obtained from independent experiments varied
less than 15%. The requirement for Mg^{2+} by both ribozymes was
studied by incubating the reaction mixtures with various
concentrations of $MgCl_2$ (1 to 500 mM) in the presence of an

20   excess of ribozyme (500 nM) over substrate (< 1nM). The
concentrations of Mg^{2+} at the half maximal velocity were
determined for both ribozymes. Determination of equilibrium
dissociation constants (K_d). For mismatched substrates which
could not be cleaved by the ribozyme, the equilibrium

25   dissociation constants were determined. Eleven different
ribozyme concentrations, ranging from 5 to 600 nM, were
individually mixed with trace amounts of end-labelled
substrates (< 1nM) in a 9 μL solution containing 50 mM Tris-
HCl pH 7.5, heated at 95°C for 2 min and cooled to 37°C for 5

30   min prior to the addition of $MgCl_2$ to a final concentration of
10 mM, in a manner similar to that of a regular cleavage
reaction. The samples were incubated at 37°C for 1.5 h, at
which 2 μL of sample loading solution (50% glycerol, 0.025% of
each bromophenol blue and xylene cyanol) was added, and the

35   resulting mixtures were electrophoresed through a
nondenaturing polyacrylamide gel (20% acrylamide with a 19:1

ratio of acrylamide to bisacrylamide, 45 mM Tris-borate buffer
pH 7.5 and 10 mM MgCl$_2$). Polyacrylamide gels were pre-run at
20 W for 1 h prior to sample loading, and the migration was
carried out at 15 W for 4.5 h at room temperature.

5 Quantification of bound and free substrates was performed
following an exposure of the gels to a phosphoimaging screen
as described earlier.

Example 3: Determination of Ribozyme and Substrate Sequence
10 **Specificity**

A number of ribozymes and substrates were made, some
of which are in accordance with the invention and others of
which are comparative examples. Analysis of the kinetic
parameters of cleavage reactions carried out using said
15 ribozymes and substrates led to the characterizations of the
method for selecting the ribozyme and substrate sequences. A
summary of the kinetic data is given below.

i)   Selection of a substrate comprising the sequence 5'-
H' GNNHNN-3' or 5'RRRH' GNNHNNN-3' and a ribozyme comprising
20 *the sequence 3'-UNNXNN-5'.*

Two forms of trans-acting delta ribozymes, δRzP1.1
and δRzP1.2 were used with their corresponding substrates
(11 nt) SP1.1 and SP1.2 for the kinetic studies (see Table 1).
The sequences of δRzP1.1 , δRzP1.2, SP1.1 and SP2.2 are given
25 in Fig. 1. δRzP1.2 differs from δRzP1.1 in that δRzP1.2 has
two nucleotides, at positions 22 and 24 of δRzP1.1,
interchanged (5'-CCCAGCU-3').

TABLE 1

Kinetic parameters	δRzP.1	δRzP.2
k_{cat} (min^{-1})	0.34 ± 0.02	0.13 ± 0.01
K_M' (nM)	17.9 ± 5.6	16.7 ± 6.4
k_{cat}/K_M' (min$^{-1} \bullet$ M^{-1})	1.89 x 10^7	0.81 x 10^7
K_{Mg} (mM)	2.2 ± 1.0	2.1 ± 0.8

Table 1. Kinetic parameters of wild type ribozyme (δRzP1.1) and mutant ribozyme (δRzP1.2). Under single turnover conditions, trace amounts of end-labelled substrate (<1 nM) were cleaved by various concentrations of ribozyme (5 to 600 nM). Reactions carried out under these conditions displayed monophasic kinetics. The values were calculated from at least two independent experiments, and standard variations were less than 15%.

In order to compare the specificity of the delta ribozyme with various substrates, δRzP1.1 was used under single turnover conditions as described above. The cleavage reactions were performed with a trace amount of each substrate (<1 nM) and 500 nM δRzP1.1. Under these conditions, the observed rates reflect the rates of cleavage without interference from either product dissociation or inhibition. For each substrate both the observed cleavage rate constants (k_{obs}) and the extent of cleavage were calculated and compared to those of the wild type substrate, as shown in Table 2.

TABLE 2

Table 2. Cleavage activity of shorter or mismatched substrates as compared to the wild type substrate (SP.1). Bold letters represent the nucleotides of wild type substrate recognized by δRzP1.1. The numbers in subscript indicate the nucleotides of wild type substrate which were individually altered to generate shorter or mismatched substrates.

Substrates	Sequence	k_{obs}^a (min^{-1})	Extent of cleavage^c (%)	k_{rel}^d	$\Delta\Delta G^{\ddagger e}$ (kcal/mol)
Wild type substrate (S11-mer)	GGGC$G_5G_6G_7U_8C_9G_{10}G_{11}$	0.34 ± 0.02		1	-
S10-mer	GGGCGGGUCG	0.022 ± 0.01	28.8 ± 4.3	0.063	-1.69
S9-mer	GGGCGGGUC	na^b	na^b	-	-
S8-mer	GGGCGGGU	na^b	na^b	-	-
SG5A	GGGCAGGUCGG	0.009 ± 0.002	20.0 ± 2.4	0.026	-2.25
SG5C	GGGCCGGUCGG	0.047 ± 0.017	1.7 ± 0.2	0.138	-1.22
SG6A	GGGCGAGUCGG	0.026 ± 0.006	5.8 ± 0.5	0.076	-1.59
SG6U	GGGCGUGUCGG	0.071 ± 0.026	3.7 ± 0.3	0.209	-0.96
SG7A	GGGCGGAUCGG	na^b	na^b	-	-
SG7U	GGGCGGUUCGG	na^b	na^b	-	-
SU8C	GGGCGGGCCGG	na^b	na^b	-	-
SU8G	GGGCGGGCGG	na^b	na^b	-	-
SC9A	GGGCGGGUAGG	0.016 ± 0.007	8.2 ± 3.0	0.047	-1.88
SC9U	GGGCGGGUUGG	0.031 ± 0.005	21.2 ± 1.0	0.091	-1.48
SG10U	GGGCGGGUCUG	0.016 ± 0.002	8.4 ± 0.5	0.047	-1.88
SG11U	GGGCGGGUCGU	0.011 ± 0.001	32.1 ± 2.5	0.032	-2.12

[a]k_{obs} is the observed rate of cleavage calculated from at least two measurements. [b]na represents no detectable cleavage activity after 3.5 hours incubation. [c]Cleavage extent (%) is obtained by fitting the data to the equation $A_t = A\infty (1-e^{-kt})$, where A_t is the percentage of cleavage at time t, $A\infty$ is the maximum percentage of the cleavage, and k is the rate constant. [d]k_{rel} is the relative rate constant as compared to that of wild type substrate. [e]$\Delta\Delta G^I$, the apparent free energy of transition-state stabilization, was calculated using the equation $\Delta\Delta G^I = RT \ln k_{rel}$, where $T = 310.15$ K ($37°C$) and $R = 1.987$ cal•K^{-1}mol^{-1}.

Further *trans*-acting *delta* ribozyme variants were
produced using plasmid pδRzP1.1. The variants have either A23
or C24 mutated to one of the other three possible bases. The
six resulting *delta* ribozyme variants are named for the
5 altered nucleotide (δRzP1-A23C, -A23G, -A23U, -C24A, -C24G,
and -C24U; Table 3). Complementary or compensatory substrates
(Table 3) were generated in which either position 7 or 8 of
the wild type substrate (SP1.1) was altered in order to
restore the Watson-Crick base pair formation of the P1 stem
10 between the substrates and the ribozyme variants.

TABLE 3

Transcripts	Sequence
Substrates	
SP1.1	$_1$GGGCGGGUCGG$_{11}$
SG7A	GGGCGGAUCGG
SG7C	GGGCGGCUCGG
SG7U	GGGCGGUUCGG
SU8A	GGGCGGGACGG
SU8C	GGGCGGGCCGG
SU8G	GGGCGGGGCGG
SU8G-9mers	$_1$GCGGGGCGG$_9$
Ribozymes	
δRzP1.1	$_{20}$CCGACCU$_{26}$
δRzP1-A23C	CCGCCCU
δRzP1-A23G	CCGGCCU
δRzP1-A23U	CCGUCCU
δRzP1-C24A	CCGAACU
δRzP1-C24G	CCGAGCU
δRzP1-C24U	CCGAUCU

15 The extent of cleavage of the δRzP1-C24N ribozyme
variants were compared with that of the wild type ribozyme
δRzP1.1 for each of 4 substrates (A), and correspondingly, the
extent of cleavage of the δRzP1-C24N ribozyme variants were

compared with that of δRzP1.1 for each of the other 4
substrates (B). The results are shown in Figure 5. The base
pair formed between the ribozyme and the substrate is
indicated by the capital and lower case letters, respectively,
on each bar of the histogram. The values are an average
calculated from at least two independent experiments.

Complementary pairs of substrates and ribozymes were
used for kinetic studies to obtain the experimental data
required for the calculation of apparent K_m (K_m') and apparent
k_2 values and the results are shown in Table 4.

24

TABLE 4

Ribozyme	k_2 (min⁻¹)	K_m' (nM)	k_2/K_m (µM⁻¹ min⁻¹)	k_{Mg} (mM)	k_d^S (nM)	k_d^P (nM)	Calculated k_d^{P1} (nM)	k_{-1} (min⁻¹)	Calculated k_1 (µM⁻¹min⁻¹)
δRzP1.1	0.34 ± 0.02	17.9 ± 5.6	19	2.2 ± 1	32 ± 3	42 ± 5	28.5	0.13 ± 0.03	4.0
δRzP1-A23Cᵃ	0.097 ± 0.01	15.5 ± 0.9	6	b—	36 ± 5	45 ± 6	1.3	ND	ND
δRzP1-A23G	0.056 ± 0.01	14.8 ± 6.4	4	5.8 ± 1	36 ± 4	74 ± 9	1.3	ND	ND
δRzP1-A23U	0.19 ± 0.01	2.5 ± 0.4	76	1.9 ± 1.2	113 ± 20	17 ± 3	25.6	0.02 ± 0.01	0.17
δRzP1-C24A	0.26 ± 0.02	102 ± 13	3	2.4 ± 1	164 ± 22	648 ± 22	734.5	0.02 ± 0.01	0.12
δRzP1-C24G	0.23 ± 0.02	13.7 ± 8.6	17	2.5 ± 0.7	40 ± 10	68 ± 9	24.3	0.15 ± 0.01	3.7
δRzP1-C24U	0.087 ± 0.01	24.6 ± 11.1	4	5.1 ± 1.5	47 ± 8	73 ± 7	530.9	ND	ND

Table 4. **Kinetic parameters for delta ribozymes.** Under single turnover conditions, the cleavage rate (k_2) and the ribozyme concentration at the half velocity (K_m') were determined. Calculated K_d^{P1} values were based on the prediction of thermodynamic stability of the P1 stem duplex (13). K_d^S and K_d^P values were determined using end-labelled uncleavable substrate analogs and synthetic reaction products.
ᵃKinetic parameters were determined using end-labeled SU8G-9mer.
ᵇThe magnesium requirement could not be obtained by fitting the experimental data to the least squares equation.
ND represents non-determined values.

ii) Selection of a substrate comprising the sequence 5'-
H' GNNHNN-3' or 5'-YHRH GNNHNNN-3'

A collection of 13 substrates including all single
mutants for positions -4 to -1 compared to the original

5   substrate were synthesized. Positions -4 to -1 refer to the
four nucleotides directly 5' to the cleavage site, position -1
being right next to the cleavage site and position -4 being
the furthest from the cleavage site, as shown in Figure 2.
For each mutant, trace amounts of 5'-^{32}P-labeled substrates (<1

10   nM) were incubated in the presence of an excess of ribozyme
(200 nM), and the maximal cleavage percentages (i.e. end-
point) (pre-steady state conditions) determined as a
comparative parameter. The Applicant observed that the base
requirement varies for each position. At position -1, the

15   base preference was A > C > U >> G, where a guanosine at this
position rendered the substrate uncleavable. At position -2,
an A improved the cleavage efficiency compared to the original
G, while a substrate with a U was poorly cleaved and a C gave
an uncleavable substrate. In contrast at position -3, C, U

20   and A gave substrates that have a two fold improved cleavage
compared to the wildtype G. Finally at position -4, the
presence of a pyrimidine (i.e. C or U) improved the maximal
percentage of cleavage by at least two fold compared to a
purine (i.e. G or A).

25   In order to assess accurately the base requirement
at each position, kinetic analysis were performed under pre-
steady-state conditions. Pseudo first-order cleavage rate
constants (k_2 and K_m') were measured with an excess of ribozyme
(5 to 600 nM) and trace amounts of end-labeled substrate (<0.1

30   nM).

TABLE 5

Position	Identity	K_M' (nM)	k_2 (min^{-1})	k_2/K_M' (nM^{-1}min^{-1})	Specificity index
-1	C	31.52	0.22	6.66×10^{-3}	1.00
	U	33.2	0.11	3.34×10^{-3}	0.50
	A	14.27	0.27	1.79×10^{-2}	2.68
	C	na	na	na	na
-2	G	31.52	0.22	6.66×10^{-3}	1.00
	A	28.7	0.33	1.15×10^{-4}	1.73
	C	na	na	na	na
	U	94	0.08	8.19×10^{-4}	0.12
-3	C	31.52	0.22	6.66×10^{-3}	1.00
	A	9.93	0.20	1.99×10^{-2}	3.02
	C	11.3	0.24	2.10×10^{-2}	3.15
	U	8.76	0.20	2.32×10^{-2}	3.48
-4	G	31.52	0.22	6.66×10^{-3}	1.00
	A	27.14	0.12	4.45×10^{-3}	0.67
	C	11.81	0.27	1.86×10^{-2}	2.79
	U	16.42	0.23	1.40×10^{-2}	2.10

Table 5. Kinetic analysis of the collection of single mutated substrates. Pseudo first-order cleavage rate constants (k_2 and K_m^1) were measured using an excess of ribozyme (5 to 600 nM) and trace amounts of end-labelled substrate (< 0.1 nM). Apparent second-order rate constants (k_2/K_m') were calculated and their relative specificity determined as compared to the original substrate. The values were calculated from at least two independent experiments, and errors were less than 25%. Sequence for position -4 to -1 are indicated for each substrate.

Then, apparent second-order rate constants (k_2/K_m') were calculated and a specificity index determined, fixing arbitrarily as 1.00 the values of the original substrate (i.e. $_{-4}GGGC_{-1}$). At position -1, the presence of a uridine resulted in a similar relative specificity (0.50) while the presence of an adenine increased the relative specificity to 2.68. This increase appears mainly as a result of a K_m' decrease of 2 fold. For position -2, the presence of a purine (i.e. G or A)

gave similar relative specificity (1.73, compared to 1.00,
respectively). In contrast, the presence of a uridine
resulted in a poorly cleaved substrate, while when a cytosine
was present, the substrate was uncleavable. In the case of

5   the uridine at position -2, the specificity was evaluated to
be reduced from 8 fold to 0.12 compared to the original
substrate (i.e. 1.00). The decrease in specificity appears to
result from a 3 fold increase of the K_m' and a 3 fold decrease
of the k_2 value. These results show a clear preference for

10   purine in position -2, and a pyrimidine should be avoided in
that position.

         For position -3, when the guanosine of the original
substrate was replaced by any other base (i.e. A, C, or U),
the K_m' was lowered by 3 fold while the k_2 remained almost

15   identical, resulting in an specificity increase ranging from
3.02 to 3.48. Finally for position -4, a purine (G and A)
yield a substrate with about the same specificity (i.e. 0.67
and 1.00). However, the presence of a pyrimidine in position
-4 improved the specificity by at least two fold with 2.79 and

20   2.10 for a C and a U, respectively. Specifically, the
presence of a C or a U the K_m' was lowered, while the k_2
remained almost identical. Thus, it appears clear that the
base requirement from position -4 to -1 of the substrate,
contributes significantly and differently to the ability of

25   the substrate to be cleaved.

         Based on the observation that mutations in position
-3 were those that most strongly increased the relative
specificity, the Applicant investigated whether or not a
larger amount of Mg^{2+} in the cleavage reaction would affect the

30   kinetic parameters of these substrates. Under single turnover
conditions, in which the ribozyme and substrate concentrations
were kept at 200 nM and 1 nM, respectively, the Applicant
found that the ribozyme cleaved these substrates at Mg^{2+}
concentrations as low as 1 mM, which is the estimated

35   physiological concentration of Mg^{2+} (Ananovoranich, S. and
Perreault, J.P. (1998) *J. Biol. Chem.*, **273**, 13182-13188, and
Trut, T.W. (1994) *Mol. Cell. Biochem.*, **140**, 1-22). A maximum

k_{obs} for each substrate was observed when the concentration of
Mg^{2+} was 10 mM. The requirement for magnesium at half-maximal
velocity (K_{Mg}) was similar for these mutated substrates and the
original substrate, varying between 1.5 to 2.2 mM. Similar
5   experiments were also performed with several other substrates
from the collection and identical results were obtained,
suggesting that the differences of the kinetic parameters for
various substrates were not related to different affinity for
the magnesium.

10   Notably, the cleavage assays performed with the
initial collection of substrates (i.e. single mutants)
indicated that the presence of a pyrimidine in the position -2
either reduces the cleavage activity or yields an uncleavable
substrate. Specifically, a uridine decreases the relative
15   specificity by 8 fold while a cytosine inhibits the cleavage
completely (see Table 6). One plausible explanation of such
results is that when a C is present at position -1 and
followed by a pyrimidine (i.e. C or U) at position -2, both
nucleotides of the substrate may interact with nucleotides
20   located on the ribozyme resulting in inactive
substrate/ribozyme complex. It seems reasonable to suggest
that base-pairing may be formed with the ribozyme guanosines
at position 27 and 28 of the J1/4 junction, which new base
pairs will compete with formation of the P1.1 stem (Fig. 2).
25   In this case, a cytosine in position -2 will form two
consecutive GC base pairs. Similarly, a uridine in position
-2 allows formation of a GC follow by a GU, which will be less
stable than two GC's, yielding a reduced activity compared to
the absence of activity. In order to learn more about the
30   nucleotide preference in position -2, taking into account the
neigboring positions, a second collection of substrates with
more than one mutation were synthesized.

          First, the Applicant verified whether a cytosine at
position -2 after non-cytosine at position -1 has a
35   detrimental effect. Based on the previous results, a substrate
with an adenine in position -1 and a cytosine in position -2,
S-$A_{-1}C_{-2}$, was synthesized and further tested for cleavage

efficiency. A moderate extent of cleavage of 14% was observed at 200 nM ribozyme, which is less than the substrates including either the sequence $C_{-1}G_{-2}$ or $A_{-1}G_{-2}$. In comparison to the substrate with the sequence $A_{-1}G_{-2}$, the $S-A_{-1}C_{-2}$ substrate

5 showed a virtually identical apparent K_M (K_M') while the cleavage constant (k_2) was reduced by approximately 4 fold, yielding a 4-fold reduction of the relative specificity (i.e. from 2.68 to 0.60; Table 6). These results suggest that the presence of a cytosine at position -2 reduces significantly

10 the cleavage of a substrate. Moreover, if this cytosine is followed by a second cytosine in position -1, the result is an uncleavable RNA molecule (see above).

TABLE 6

Mutant	Km' (nM)	k_2 (min^{-1})	K_2/KM' (nM^{-1}min^{-1})	Specificity index
$SC_{-1}G_{-2}$	31.5	0.22	6.98×10^{-3}	1
SA_{-1}	14.3	0.27	1.89×10^{-2}	2.68
$SA_{-1}C_{-2}$	15.4	0.06	3.9×10^{-3}	0.6
$SA_{-1}C_{-2}C_{-3}$	15.2	0.039	2.57×10^{-3}	0.4
$SA_{-1}C_{-2}C_{-3}C_{-4}$	16.5	0.25	1.52×10^{-2}	2.28

15

Table 6. Kinetic analysis of the collection of multiple mutated substrates. Pseudo first-order cleavage rate constants (k_2 and K_m') were measured using an excess of ribozyme (5 to 600 nM) and trace amounts of end-labelled

20 substrate (<0.1 nM). Apparent second-order rate constants (k_2/K_m') were calculated and their relative specificity determined as compared to the original experiments, and errors were less than 25%. Sequence for position -4 to -1 are indicated for each substrate.

25

Secondly, the Applicant verified whether a cytosine at position -2 followed by a cytosine at position -3 gives a cleavable substrate. In other words, two consecutive

30 cytosines, regardless of their positions, will yield uncleavable substrates. Therefore, the Applicant synthesized the substrate $S-A_{-1}C_{-2}C_{-3}$ and verified its ability to be cleaved. The $S-A_{-1}C_{-2}C_{-3}$ put together was cleaved with kinetic parameters

almost identical to the the substrate $S-A_{-1}C_{-2}$ substrate except
that the k_2 was slightly reduced to 0.039 min^{-1} compared to
0.062 min^{-1}, resulting in a small reduction of the relative
specificity (i.e. from 0.60 to 0.40; Table 6). These results

5   show that the presence of a cytosine at position -3 following
a cytosine at position -2 reduced slightly the cleavage
activity, and did not significantly modify the ability of a
substrate to be cleaved. Thus, a cytosine at position -3 does
not have the same influence as that at position -2.

10   Thirdly, the Applicant asked whether two consecutive
cytosines at positions -4 and -3 give a similar effect
yielding uncleavable (or less cleaved) substrate. A substrate
containing cytosines at positions -3 and -4 and adenines in
position -1 and -2 was synthesized. Adenines were included in

15   position -1 and -2 because this residue appears to give a
readily cleaved substrate as compared to the single mutation
collection (see above). The $S-A_{-1}A_{-2}C_{-3}C_{-4}$ mutant has a maximum
cleavage of 61%. Moreover, the Applicant determined a K_M' of
16.5 nM and a k_2 value increased to 0.25 min^{-1}, resulting in a

20   substrate with a relative specificity of 2.28 as compared to
the original substrate (Table 6). Thus, the presence of two
consecutive cytosines at position -3 and -4 has no detrimental
effect.

          Finally, the Applicant asked whether it is possible

25   to compensate for the detrimental effect of the presence of
two consecutive cytosines at positions -1 and -2, by including
the one at position -2 in a hairpin structure. A longer RNA
substrate (i.e. 18-mer compared to 14mer) including a hairpin
at 5'-end, which involved the C_{-2} in the last base pair of the

30   helix was chemically synthesized and then tested. This
substrate was poorly cleaved. Only trace amounts of products
were detected (i.e. maximum percentage cleavage of <2.0 %),
and as a consequence, no more extensive characterization was
possible. If the sequence was drawn in order to avoid the

35   formation of the 5'-end hairpin (i.e. C_{-2} remains single
strand; S-hp-), no cleavage at all was observed. These two
results showed that the presence of a base-paired cytosine at

position -2 gave minimal activity as compared to this cytosine in single strand. However, the improvement was very limited.

Example 4: L4 loop Modifications

A modified form of δRzP1.1 described above was made by replacing the L4 loop sequence GCUU which is relatively unstable, with the ultrastable L4 loop (UUCG) (shown on the right in Figure 3). The kinetic parameters (k_{cat} and K_M) and dissociation constant (K_d) were virtually identical.

Example 5: Bimolecular ribozyme

A modified form of δRzP1.1 described above was made by dividing the L4 loop into two resulting in two fragments, namely, RzA and RzB (as shown in Figure 4). The RzA consists of 37 nucleotides encompassing a substrate recognition site (P1 stem), P3 stem and portions of P2 and P4 stems. The RzB consists of 20 nucleotides which is able to base pair to RzA to form a bimolecular ribozyme complex. RzA and RzB were synthesized as described in Example 1. Because both RzA and RzB are relatively small, they can be chemically synthesized. Therefore, this bimolecular delta ribozyme allows the introduction of any chemically modified nucleoside.

Example 6: Deoxyribonucleotide modifications

Example 5 describes a bimolecular ribozyme. Modified versions of the ribozyme described in Example 5 were made by replacing one ribonucleotide in RzB with a deoxyribonucletide individually at positions 9 to 15. This resulted in 7 different RzB's each containing one deoxyribonucleic acid.

The influence of 2'-OH groups in RzB on the catalytic activity of RzA:RzB complex was analyzed. 0.066 uM of a mix of cold and end-labeled RNA substrates were incubated in presence of 0.066 uM of RzA and 0.2 uM of various RzB RNA/DNA mixed polymers. The incubation was performed in 50 mM Tris-HCl pH 8.0 and 50 mM $MgCl_2$ at 37°C. An aliquot was

removed after one hour and the reaction stopped by the
addition of an excess of stop solution (xc, bb, formamide).
Reaction mixtures were fractioned on 20% polyacrylamide gel
electrophoresis and were exposed on x-ray films. Fully
5   deoxyribonucleotide RzB molecules are not able to support a
cleavage activity. Individual deoxy substitution mutants were
subjected to catalytic cleavage. All of the reconstituted
complexes were active to different extents. S and P
respectively represent substrate and product species. As an
10 example, dGg stands for GGCGCAUGgCUAAGGGACCC where uppercase
and lowercase letters respectively represent ribo- and
deoxyribonucleotides. The results are shown in Figure 6 and
Table 7.

        Table 7 shows the quantification of time course
15 experiments performed. Rate and extent of cleavage values
were obtained from fitting the experimental data to the
equation $A_t = A_{alpha} (1-e-kt)$ were A_t is the percentage of
cleavage at time, t, A_{alpha} is the maximum cleavage and k is the
reaction rate. Data analysis was performed with GraFit
20 Version 3.01 from Erithacus Software.

TABLE 7

Species	Rate (min^{-1})	Extent (%)
RzB	5.7×10^{-2}	27.01
dG9	3.3×10^{-2}	9.80
dC10	2.4×10^{-2}	30.42
dU11	4.6×10^{-2}	45.87
dA12	4.0×10^{-2}	26.79
dA13	1.8×10^{-2}	27.46
dG14	8.0×10^{-2}	61.44
dG15	7.8×10^{-2}	54.15

Table 7. Rate and extent of substrate cleavage using 2'-OH
25 modified ribozymes.

Figure 6 illustrates the sequence of the ribozymes of this Example and shows the efficiency of cleavage of the substrate molecules as a function of the position of the deoxyribonucleic acid.

5

Example 7: Cleavage of HDAg mRNA.

Plasmids encoding the HDAg mRNA and delta ribozymes. The pKSAgS plasmid carries the S-HDAg mRNA in pBluescript KS+ (Stratagene). Briefly, the S-HDAg mRNA insert (positions 900

10 to 1679 of the vHDV.5 variant (according to Lafontaine, D., Mercure, S. and Perreault, J.-P. (1997) *Nucleic Acids Res.*, **25**, 123-125) were retrieved by PCR amplification using pSVL(AgS) (Chao, M., Hsieh, S.Y. and Taylor, J. (1990) *J. Virol.*, **64**, 5066-5069) as template. The oligonucleotides used

15 in this PCR had restriction sites situated at their 5' ends so as to facilitate subsequent cloning: HDV1679.66: 5'CC<u>GGATCC</u>CTCGGGCTCGGGCG 3' (underlined is the *Bam* H1 restriction site) and HDV900.914: 5'CC<u>AAGCTT</u>CGAAGAGGAAAGAAG 3' (underlined is the *Hind* III restriction site). Plasmid DNA

20 (pSVL(AgS), 50 ng), 0.4 mM of each oligonucleotide, 200 mM dNTPs, 1.25 mM MgCl$_2$, 10 mM Tris-HCl pH 8.3, 50 mM KCl, and 1 U Taq DNA polymerase were mixed together in a final volume of 100 μL. The Applicant performed one low stringent PCR cycle (94°C for 5 min, 53°C for 30 s, 72°C for 1 min), followed by

25 35 cycles at higher stringency (94°C for 1 min, 62°C for 30 s, 72°C for 1 min). The mixture was fractionated by electro- phoresis in a 1% agarose gel in 1X TBE buffer (90 mM Tris- borate, 2 mM EDTA pH 8.0), the expected band excised and eluted using the QIAquick gel extraction kit (Qiagen), and

30 finally digested and ligated into pBluescript KS+. The strategy used for the construction of plasmids carrying ribozymes with modified substrate recognition domains is described above. All constructs were verified by DNA sequencing.

35 *RNA Synthesis. In vitro transcription*: HDAg mRNA was transcribed from *Hind* III-linearized pKSAgS, while ribozymes were transcribed from *Sma* I-linearized ribozyme

encoding plasmids as described in Example 1. Small substrates
(11-nt) were synthesized as described in Example 1.

   Oligonucleotide probing. DNA oligonucleotides
complementary to the potential target sites were purchased

5 from Gibco-BRL and 5'-end labelled using T4 polynucleotide
kinase (Pharmacia) in the presence of 10 µCi [γ-^{32}P]ATP.
Labelled oligonucletiodes (~ 2 500 cpm; ~ 0.05 nM) and
unlabelled mRNA (2.4 to 1 200 nM) were hybridized together for
10 min at 25°C in a solution containing 50 mM Tris-HCl pH 7.5

10 and 10 mM MgCl$_2$ in a final volume of 15 µl. Loading solution
(2 µL of 1X TBE, 10 mM MgCl$_2$, 40% glycerol, 0.25% bromophenol
blue and 0.25% xylene cyanol) was added, and the resulting
solutions fractionated on native 5% PAGE gels (30:1 ratio of
acrylamide to bisacrylamide, 50 mM Tris-borate pH 8.3, 10 mM

15 MgCl$_2$ and 5% glycerol) at 4°C in the presence of recirculating
50 mM Tris-borate pH 8.3 and 10 mM MgCl$_2$ buffer. The dried
gels were analyzed with the aid of a PhosphorImager (Molecular
Dynamics). RNase H probing was performed using the same
oligonucleotides. In these experiments randomly labelled S-

20 HDAg mRNA (~10 000 cpm; ~10 nM) and unlabelled oligo-
nucleotides (1 µM) were annealed as described for gel shift
assays for 10 min, then 0.2 U of *E. coli* RNase H (Pharmacia)
was added and the reaction incubated at 37°C for 20 min. The
reactions were stopped by the addition of stop-solution (3 µL

25 of 97% formamide, 10 mM EDTA, 0.25% bromophenol blue and 0.25%
xylene cyanol), fractionated on 5% denaturing PAGE gels, and
analyzed by autoradiography.

   In vitro cleavage assays and kinetic analyses.
Cleavage assays were performed at 37°C under single turnover
30 conditions with either randomly labelled mRNA (~ 10 nM) or 5'-
end labelled small substrates (<1nM), and an excess of
ribozyme (2,5 µM) in 10 µL final volume containing 50 mM Tris-
HCl pH 8.0 and 10 mM MgCl$_2$. A pre-incubation of 5 min at 37°C
preceeded the addition of the Tris-magnesium buffer which
35 initiates the reaction. After an incubation of 1 to 3 hrs at
37°C, stop-solution (5µl) was added and the mixture quickly

stored at -20°C until its fractionation on 5% denaturing PAGE
gels and subsequent autoradiography. Cleavage sites of the
active ribozymes were verified by primer extension assays as
described previously (Côté, F. and Perreault, J.-P. (1997) *J.*
5   *Mol. Biol.*, **273**, 533-543). Briefly, oligonucleotides were
synthesized to have complementary sequence to positions
downstream (~ 100 positions) from the cleavage site according
to the mRNA. For example, for the cleavage site of Rz-12, the
oligonucleotide primer, 5'CTTTGATGTTCCCCAGCCAGG-3' (21mer),
10   was used in the reverse transcriptase reaction containing the
ribozyme cleavage reaction mixture.

      Active ribozymes (Rz-1, -11 and -12) were
characterized under single turnover conditions essentially as
described in Example 1.

36

TABLE 8

Ribozyme	P1 stem sequence	Size of expected cleavage products (nt)	
Rz-1	CCCAGCU	265	551
Rz-2	CCUCUUU	330	486
Rz-3	CCUUGUU	403	413
Rz-4	UGUUCUU	440	376
Rz-6	GGGGUUU	572	244
Rz-7	UCCCCUU	593	223
Rz-9	GGACUCU	640	176
Rz-11	UCGACUU	130	686
Rz-12	GCCACCU	175	641

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TABLE 8 (cont'd)

mRNA sequence

1	CACCGCGGU	GCGGCCGC	UAGAACUAG	GGAUCCCU	GGCUCGGGCG	GCGAGUCC
61	CAGUCUCCU	UUUACAGA	AUGUAAGAG	ACUGAGGA	GCCGCCUCUA	GCCGAGAU
121	GCCGGUCCG	GUCGAGGA	AACCGCGGA	GGAGAGAA	GAUCCUCGAG	CAGUGGGU	(11,12)
181	CCGGAAGAA	GAAGUUAG	GAACUCGAG	GAGACCUC	GAAGACAAAG	AAGAAACU
241	AGAAGAUAG	GGACGAAA	CCCUGGCUG	GGAACAUC	AGGAAUUCUC	GGAAAGAA	(1)
301	AUAAGGAUG	AGAGGGGG	CCCCCCGCG	AGAGGGCC	AACGGACCAG	AUGGAGGU	(2)
361	ACUCCGGAC	UCGGAAGA	CCUCUCAGG	GAGGAUUC	CGACAAGGAG	AGGCAGGA	(3)
421	CCGACGAAG	AAGGCCCU	AGAACAAGA	GAAGCAGC	UCGGGCGGGAG	GCAAGAAC	(4)
481	CAGCAAGGA	GAAGAAGA	AACUCAGGA	GUUGACCG	GAAGACGAGA	GAAGGGAA
541	AAGAGUAGC	GGCCCGCC	UUGGGGGUG	GAACCCCC	GAAGGUGGAU	CGAGGGGA	(6,7)
601	GCCCGGGGG	GGCUUCGU	CCAAUCUGC	GGGAGUCC	GAGUCCCCU	UCUCUCGG	(9)
661	CGGGGAGGG	CUGGACAU	GGGGAAACC	GGGAUUUC	UAGGAUAUAC	UCUUCCCA
721	CGAUCCGCC	UUUUCUCC	AGAGUGUC	ACCCCAGU	AUAAAGCGGG	UUUCCACU
781	CAGGUUUGC	UCUCGCGGU	UUCUUUCCU	UUC

Table 8. Synthesized delta ribozyme. Previous page is the ribozyme nomenclature with the sequence composing the P1 stem domain and the size of the expected products. This page is the mRNA sequence. The mRNA sequences targeted by ribozymes are underlined, and the ribozyme number is in parentheses on the right.

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Of the nine ribozymes examined, three, namely Rz1,
Rz11, and Rz12, specifically cleaved a derivative HDV mRNA.
The most active ribozyme under steady-state conditions,
displaying multiple turnovers, was Rz-12. As can be observed
5   from Table 8, the sequence of the substrate for this ribozyme
(positions 87-97) is 5'CAGU GGGUGG-3'. This accords with the
sequence preferences shown in Table 5.

Example 8: Cleavage Assay of a ribozyme of the invention
10   **against 552 nt-HBV RNA substrate.**

500 nM of a *delta* ribozyme as shown in Figure 7 was
incubated with 1 nM randomly-labelled 552 nt-HBV (human
hepatitis B virus) mRNA at 37°C in the presence of 50 mM Tris-
HCl pH 7.5 and 10 mM $MgCl_2$. A single exponential equation was
15   used to fit data to k_{obs} = 0.031 min^{-1} with 28% cleavage. This
demonstrates that a ribozyme of the invention cleaves mRNA
from the human hepatitis B virus.